

1 Paper No. \_\_\_\_\_

2 Filed on behalf of: Senior Party Genetics Institute, LLC

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9 UNITED STATES PATENT AND TRADEMARK OFFICE

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11 BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES

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12

13 Stryker Corporation,  
Junior Party,  
(Patent 5,266,683,

14 Inventors: Hermann Oppermann, Engin Ozkaynak, Thangavel Kuberasampath,  
David C. Rueger, Roy H.L. Pang),

15 v.

16

17 Genetics Institute, LLC,  
Senior Party,

18 (Application 08/319,831,

Inventors: Rodney M. Hewick, Jack H. Wang,  
John M. Wozney, Anthony J. Celeste).

20

21 Patent Interference 105,508 (RES)  
(Technology Center 1600)

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23 GENETICS INSTITUTE CLEAN COPY OF CLAIMS

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1 Pursuant to the Notice Declaring Interference dated October 6, 2006, Paper No. 1, the  
2 party Genetics Institute, LLC, submits a clean copy of its involved claims pending as of the time  
3 of the declaration of this interference.

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Respectfully submitted,

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9 Dated: October 20, 2006

By: / Kenneth J. Meyers /  
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10

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1 PATENT INTERFERENCE 105,508 (RES)

2 Genetics Institute, LLC,  
3 Senior Party,  
4 (Application 08/319,831,  
Inventors: Rodney M. Hewick, Jack H. Wang,  
John M. Wozney, Anthony J. Celeste).

5 CLEAN COPY OF CLAIMS

- 6 1. A purified BMP-8 protein characterized by:
- 7 (a) at least one of the following sequences:
- 8     i) Arg-His-Glu-Leu-Tyr-Val-Ser-Phe-Gln-Asp-Leu-Gly-Trp-Leu-Asp-Trp-  
9         Val-Ile-Ala-Pro-Gln-Gly-Tyr (SEQ ID NO: 1);
- 10     ii) Leu-Ser-Ala-Thr-Ser-Val-Leu-Tyr-Tyr-Asp-Ser-Ser-Asn-Asn-Val-Ile-  
11         Leu-Arg (SEQ ID NO: 2); and
- 12     iii) Ala-Cys-Cys-Ala-Pro-Thr-Lys (SEQ ID NO:3);
- 13 (b) a molecular weight of 28,000 - 38,000 daltons as determined by sodium dodecyl  
14 sulfate polyacrylamide gel electrophoresis; and
- 15 (c) a molecular weight of 14,000 - 20,000 daltons under reducing conditions as  
16 determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis said  
protein being a disulfide linked dimer wherein each of the subunits contains the  
formation of cartilage and/or bone.
- 17 26. A pharmaceutical formulation for bone and/or cartilage formation comprising an  
effective amount of a BMP-8 protein of claim 1 in a pharmaceutically acceptable vehicle.
- 18 27. A composition of claim 26 further comprising a matrix for supporting said composition  
and providing a surface for bone and/or cartilage formation.
- 19 28. The composition of claim 27 wherein said matrix comprises a material selected from the  
group consisting of hydroxyapatite, collagen, polylactic acid and tricalcium phosphate.
- 20 29. A pharmaceutical composition for wound healing and tissue repair said composition  
21 comprising an effective amount of a BMP-8 protein of claim 1 in a pharmaceutically acceptable  
vehicle.
- 22
- 23
- 24

**CERTIFICATE OF SERVICE**

I hereby certify that a copy of the foregoing was served on the party Stryker Corporation through its attorney of record on this the 20<sup>th</sup> day of October, 2006 as follows:

VIA FEDERAL EXPRESS

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Filed on behalf of: Stryker Corporation

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UNITED STATES PATENT AND TRADEMARK OFFICE

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BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES

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**STRYKER CORPORATION,**

Junior Party

(Patent 5,266,683,

Inventors: Hermann Oppermann, Engin Ozkaynak, Thangavel Kuberasanpath,  
David C. Rueger, Roy H.L. Pang),

v.

**GENETICS INSTITUTE, LLC,**

Senior Party

(Application 08/319,831,

Inventors: Rodney M. Hewick, Jack H. Wang,  
John M. Wozney, Anthony J. Celeste).

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Patent Interference No. 105,508 (RES)

(Technology Center 1600)

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STRYKER CORPORATION'S CLEAN COPY OF CLAIMS AND SEQUENCES

STRYKER CORPORATION'S CLEAN COPY OF CLAIMS AND SEQUENCES

- 1 Pursuant to Bd. R. 110(a), Junior Party Stryker Corporation ("Stryker") submits the
- 2 following clean copy of its involved claims of U.S. Patent 5,266,683. Junior Party Stryker also
- 3 submits herewith a clean copy of the sequences recited in the involved claims.

- 1        21. An isolated protein comprising the amino acid sequence described by residues  
2                  306 to 402 of Seq. ID No. 28.
- 3
- 4        22. The protein of claim 21 comprising the amino acid sequence described by  
5                  residues 270-402 of Seq. ID No. 28 (hOP2-Arg).
- 6
- 7        23. The protein of claim 22 comprising the amino acid sequence described by  
8                  residues 267 to 402 of Seq. ID No. 28 (hOP2-Pro).
- 9
- 10       24. The protein of claim 23 comprising the amino acid sequence described by  
11                  residues 264 to 402 of Seq. ID No. 28 (hOP2-Ala).
- 12
- 13       25. The protein of claim 24 comprising the amino acid sequence described by  
14                  residues 243 to 402 of Seq. ID No. 28 (hOP2-Ser).
- 15
- 16       26. The protein of claim 25 comprising the amino acid sequence described by  
17                  residues 1 to 402 of Seq. ID No. 28 (hOP2-PP).
- 18
- 19       27. The protein of claim 6, 15, 18 or 21 capable of inducing cartilage and bone  
20                  formation when implanted in a mammal in association with a matrix.
- 21
- 22       28. Osteogenic protein expressed from recombinant DNA in a host cell,  
23                  the protein comprising a pair of oxidized subunits disulfide bonded to  
24                  produce a dimeric species, one of said subunits having an amino acid sequence  
25                  sufficiently duplicative of the sequence comprising residues 335 to 431 of Seq. ID  
26                  No. 1 (OPS),  
27                  such that the disulfide bonded dimeric species comprising said subunit has  
28                  a conformation capable of inducing cartilage and endochondral bone formation in  
29                  a mammal when disposed within a matrix implanted in said mammal.
- 30
- 31       29. Osteogenic protein expressed from recombinant DNA in a host cell,

1                   the protein comprising a pair of oxidized subunits disulfide bonded to  
2                   produce a dimeric species, having a conformation capable of inducing cartilage  
3                   and endochondral bone formation in a mammal when disposed within a matrix  
4                   implanted in said mammal,

5                   one of said subunits having an amino acid sequence encoded by a nucleic  
6                   acid capable of hybridizing to a nucleic acid encoding OPS (res. 335-431, Seq. ID  
7                   ID No. 1) under stringent hybridization conditions.

8  
9                 39. The protein of claim 28 or 29 wherein said subunit comprises at least the  
10                  osteogenically active region of a protein selected from the group consisting of:  
11                  mOP1-PP (residues 1-430, Seq. ID No. 24); mOP2-PP (residues 1-399 of Seq. ID  
12                  ID No. 26); and hOP2-PP (residues 1-402 of Seq. ID No. 28).

13  
14                 45. An isolated polypeptide chain useful as a subunit of a dimeric osteogenic protein,  
15                  said polypeptide chain having an amino acid sequence sharing greater than 74%  
16                  identity with the sequence described by residues 264-402 of Seq. ID No. 28  
17                  (hOP2-Ala) such that the disulfide bonded dimeric species comprising said  
18                  polypeptide chain is capable of inducing endochondral bone formation when  
19                  implanted in a mammal in association with a matrix.

20  
21                 46. An isolated polypeptide chain useful as a subunit of a dimeric osteogenic protein  
22                  having a conformation capable of inducing endochondral bone formation in a  
23                  mammal when implanted in a mammal in association with a matrix,

24                  said polypeptide chain having an amino acid sequence encoded by a  
25                  nucleic acid capable of hybridizing to a nucleic acid encoding the pro region of  
26                  mOP2-PP (res. 17-260 of Seq. ID No. 26) or hOP2-PP (res. 17-263 of Seq. ID  
27                  No. 28) under stringent hybridization conditions.

28  
29                 47. The polypeptide chain of claim 45 or 46 having an amino acid sequence sharing  
30                  greater than 80% identity with the amino acid sequence of hOP2-Ala.

- 1           48. The polypeptide chain of claim 47 having an amino acid sequence sharing greater  
2           than 85% identity with the amino acid sequence of hOP2-Ala.  
3  
4           49. The polypeptide chain of claim 45 or 46 wherein said amino acid sequence is  
5           selected from the group consisting of: mOP2-Ala (residues 261-399 Seq. ID No.  
6           26); hOP2-Ala (residues 264-402 of Seq. ID No. 28); hOP2-Pro (residues 267-  
7           402 of Seq. ID No. 28); hOP2-Arg (residues 270-402 of Seq. ID No. 28) and  
8           hOP2-Ser (residues 243-402 of Seq. ID No. 28).  
9  
10          50. The polypeptide chain of claim 45 or 46 wherein said amino acid sequence is  
11          derived from an amino acid sequence selected from the group consisting of:  
12          mOP2-PP (residues 1-399 of Seq. ID No. 26) and hOP2-PP (residues 1-402 of  
13          Seq. ID No. 28) including allelic variants thereof, and natural and biosynthetic  
14          mutants thereof.  
15  
16          51. The polypeptide chain of claim 45 or 46 that is glycosylated.  
17  
18          52. An isolated dimeric protein capable of inducing cartilage or endochondral bone  
19          formation in a mammal when implanted in said mammal in association with a  
20          matrix,  
21                 said protein comprising a pair of disulfide-bonded polypeptide chains  
22                 constituting a dimeric species, wherein each said polypeptide chain is the  
23                 polypeptide chain of claim 45 or 46.  
24  
25          53. The dimeric protein of claim 52 wherein each said polypeptide chain is  
26          independently selected and comprises at least the osteogenically active region of  
27          mOP2-PP (residues 1-399 of Seq. ID No. 26) or hOP2-PP (residues 1-402 of Seq.  
28          ID No. 28).  
29  
30          54. The dimeric protein of claim 53, wherein each said polypeptide chain is  
31          independently selected from the group consisting of: mOP2-Ala (residues 261-  
32          399 Seq. ID No. 26); hOP2-Ala (residues 264-402 of Seq. ID No. 28); hOP2-Pro

- 1                   (residues 267-402 of Seq. ID No. 28); hOP2-Arg (residues 270-402 of Seq. ID  
2                   No. 28) and hOP2-Ser (residues 243-402 of Seq. ID No. 28).
- 3
- 4       58. A protein expressed from recombinant DNA in a host cell, said protein  
5                   comprising an amino acid sequence encoded by a nucleic acid capable of  
6                   hybridizing to a nucleic acid encoding residues 306-402 of hOP2 (Seq. ID No. 28)  
7                   under stringent hybridization conditions.
- 8
- 9

Interference No. 105,508 (RES)  
STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1  
2  
3 SEQUENCE DESCRIPTION: SEQ ID NO:1:  
4  
5 GGTGCGGGCC CGGAGGCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGGG ATG CAC GTG 57  
6 Met His Val  
7 1  
8  
9 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA 105  
10 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala  
11 5 10 15  
12  
13 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC 153  
14 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn  
15 20 25 30 35  
16  
17 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG 201  
18 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg  
19 40 45 50  
20  
21 CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC 249  
22 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg  
23 55 60 65  
24  
25 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG 297  
26 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met  
27 70 75 80  
28  
29 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC 345  
30 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly  
31 85 90 95  
32  
33 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC 393  
34 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly  
35 100 105 110 115  
36  
37 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC 441  
38 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp  
39 120 125 130  
40  
41 ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC 489  
42 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe  
43 135 140 145  
44  
45 CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC 537  
46 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile  
47 150 155 160  
48  
49 CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC 585  
50 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp  
51 165 170 175  
52  
53 TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT 633  
54 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr  
55 180 185 190 195  
56  
57 CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC 681

Interference No. 105,508 (RES)  
 STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu			
2	200	205	210	
3				
4	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC		729	
5	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp			
6	215	220	225	
7				
8	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG		777	
9	lle Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu			
10	230	235	240	
11				
12	GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC		825	
13	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro			
14	245	250	255	
15				
16	AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC		873	
17	Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro			
18	260	265	270	275
19				
20	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC		921	
21	Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile			
22	280	285	290	
23				
24	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC		969	
25	Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro			
26	295	300	305	
27				
28	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC		1017	
29	Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser			
30	310	315	320	
31				
32	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC		1065	
33	Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe			
34	325	330	335	
35				
36	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC		1113	
37	Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala			
38	340	345	350	355
39				
40	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG		1161	
41	Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met			
42	360	365	370	
43				
44	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC		1209	
45	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn			
46	375	380	385	
47				
48	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC		1257	
49	Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala			
50	390	395	400	
51				
52	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA		1305	
53	lle Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys			
54	405	410	415	
55				
56	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC		1351	
57	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His			
58	420	425	430	

Interference No. 105,508 (RES)  
STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1 GAGAATTCAG ACCCTTTGGG GCCAAGTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG 1411  
2 GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG 1471  
3 TGAGAGATA TTAGGAAACA TGAGCAGCAT ATGGCTTTG ATCAGTTTT CAGTGGCAGC 1531  
4 ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAGAACCC TAGCAGGAAA AAAAACAAAC 1591  
5 GCATAAAGAA AAATGGCCGG GCCAGGTCA TGGCTGGAA GTCTCAGCCA TGCACGGACT 1651  
6 CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711  
7 GGGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771  
8 CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21 SEQUENCE DESCRIPTION: SEQ ID NO:24:  
22  
23 CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCCTCCGCTG CCACCTGGGG 60  
24 CGGCGCGGGC CCGGTGCCCG GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC 115  
25 Met His Val Arg  
26 1  
27  
28 TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT 163  
29 Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro 30  
30 5 10 15 20  
31  
32 CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG 211  
33 Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu 35  
34 25 30 35  
35  
36 GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG 259  
37 Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg 40  
38 40 45 50  
39  
40 GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CCG 307  
41 Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro 45  
42 55 60 65  
43  
44 CGC CCG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG 355  
45 Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu 47  
46 70 75 80  
47  
48 GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG ACC GGG CCG GAC GGA CAG 403  
49 Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln 52  
50 85 90 95 100  
51  
52 GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT 451  
53 Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro 55  
54 105 110 115  
55  
56  
57 TTA GCC AGC CTG CAG GAC AGC CAT TTC CTC ACT GAC GCC GAC ATG GTC 499  
58 Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val

Interference No. 105,508 (RES)  
 STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

	120	125	130	
1				
2				
3	ATG AGC TTC GTC AAC CTA GTG GAA CAT GAC AAA GAA TTC TTC CAC CCT			547
4	Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro			
5	135	140	145	
6				
7	CGA TAC CAC CAT CGG GAG TTC CGG TTT GAT CTT TCC AAG ATC CCC GAG			595
8	Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu			
9	150	155	160	
10				
11	GGC GAA CGG GTG ACC GCA GCC GAA TTC AGG ATC TAT AAG GAC TAC ATC			643
12	Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile			
13	165	170	175	180
14				
15	CGG GAG CGA TTT GAC AAC GAG ACC TTC CAG ATC ACA GTC TAT CAG GTG			691
16	Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr Val Tyr Gln Val			
17	185	190	195	
18				
19	CTC CAG GAG CAC TCA GGC AGG GAG TCG GAC CTC TTC TTG CTG GAC AGC			739
20	Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser			
21	200	205	210	
22				
23	CGC ACC ATC TGG GCT TCT GAG GAG GGC TGG TTG GTG TTT GAT ATC ACA			787
24	Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr			
25	215	220	225	
26				
27	GCC ACC AGC AAC CAC TGG GTG GTC AAC CCT CGG CAC AAC CTG GGC TTA			835
28	Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu			
29	230	235	240	
30				
31	CAG CTC TCT GTG GAG ACC CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG			883
32	Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu			
33	245	250	255	260
34				
35	GCA GGC CTG ATT GGA CGG CAT GGA CCC CAG AAC AAG CAA CCC TTC ATG			931
36	Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met			
37	265	270	275	
38				
39	GTG GCC TTC TTC AAG GCC ACG GAA GTC CAT CTC CGT AGT ATC CCG TCC			979
40	Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg Ser Ile Arg Ser			
41	280	285	290	
42				
43	ACG GGG GGC AAG CAG CCC AGC CAG AAT CGC TCC AAG ACG CCA AAG AAC			1027
44	Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn			
45	295	300	305	
46				
47	CAA GAG GCC CTG AGG ATG GCC AGT GTG GCA GAA AAC AGC AGC AGT GAC			1075
48	Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser Asp			
49	310	315	320	
50				
51	CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC			1123
52	Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp			
53	325	330	335	340
54				
55	CTT GGC TGG CAG GAC TGG ATC ATT GCA CCT GAA GGC TAT GCT GCC TAC			1171
56	Ley Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr			
57	345	350	355	
58				

1	TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC	1219
2	Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala	
3	360 365 370	
4		
5	ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC	1267
6	Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp	
7	375 380 385	
8		
9	ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT	1315
10	Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser	
11	390 395 400	
12		
13	GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA	1363
14	Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg	
15	405 410 415 420	
16		
17	AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTCC TGAGACCTG	1413
18	Asn Met Val Val Arg Ala Cys Gly Cys His	
19	425 430	
20		
21	ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTC ACCATCTAAG TCTCTCACTG	1473
22		
23	CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCGTAGCC TTCCCTCACCC TCCCAACCGG	1533
24		
25	AAGCATGTAA GGGTTCAGA AACCTGAGCG TGCAAGCAGCT GATGAGCGCC CTTTCTCT	1593
26		
27	GGCACGTGAC GGACAAGATC CTACCAGCTA CCACAGAAA CGCCTAAGAG CAGGAAAAT	1653
28		
29	GTCTGCCAGG AAAGTGTCCA GTGTCACAT GGCCCCCTGGC GCTCTGAGTC TTTGAGGAGT	1713
30		
31	AATCGCAAGC CTCGTTCAAGC TGCAAGCAGAA GGAAGGGCTT AGCCAGGGTG GGCGCTGGCG	1773
32		
33	TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAACCCAT	1833
34		
35	GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATT	1873
36		
37		
38		
39		
40	<b>SEQUENCE DESCRIPTION: SEQ ID NO:26:</b>	
41		
42	gaattccgct gccaggcaca ggtgcggcgat ctggtcctcc cccgtctggcg tcagccgagc	60
43		
44	ccgaccagct accagtggat ggcgcggc tgaaagtccg ag atg gct atg cgt	114
45	Met Ala Met Arg	
46	1	
47		
48	ccc ggg cca ctc tgg cta ttg ggc ctt gct ctg tgc gcg ctg gga ggc	162
49	Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly	
50	5 10 15 20	
51		
52	ggc cac ggt ccc ggt ccc ccg cac acc tgt ccc cag cgt cgc ctg gga	210
53	Gly His Gly Pro Gly Pro His Thr Cys Pro Gln Arg Arg Leu Gly	
54	25 30 35	
55		
56	gcg cgc gac cgg gac atg cag cgt gaa atc ctg ccg gtg ctc ggg cta	258
57	Ala Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro Val Leu Gly Leu	
58	40 45 50	

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1					
2	ccg gga cgc ccc gac ccc gtg cac aac ccg ccg ctg ccc ggc acg cag				306
3	Pro Gly Arg Pro Asp Pro Val His Asn Pro Pro Leu Pro Gly Thr Gln				
4	55	60	65		
5					
6	cgt gcg ccc ctc ttc atg ttg gac cta tac cac gcc atg acc gat gac				354
7	Arg Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr Asp Asp				
8	70	75	80		
9					
10	gac gac ggc ggg cca cca cag gct cac tta ggc cgt gcc gac ctg gtc				402
11	Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp Leu Val				
12	85	90	95	100	
13					
14	atg agc ttc gtc aac atg gtg gaa cgc gac cgt acc ctg ggc tac cag				450
15	Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly Tyr Gln				
16	105	110	115		
17					
18	gag cca cac tgg aag gaa ttc cac ttg gac cta acc cag atc cct gct				498
19	Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile Pro Ala				
20	120	125	130		
21					
22	ggg gag gct gtc aca gct gct gag ttc cgg atc tac aaa gaa ccc agc				546
23	Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro Ser				
24	135	140	145		
25					
26	acc cac ccg ctc aac aca acc ctc cac atc agc atg ttc gaa gtg gtc				594
27	Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu Val Val				
28	150	155	160		
29					
30	caa gag cac tcc aac agg gag ttc gac ttg ttc ttt ttg gat ctt cag				642
31	Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Leu Asp Leu Gln				
32	165	170	175	180	
33					
34	acg ctc cga tct ggg gac gag ggc tgg ctg gtg ctg gac atc aca gca				690
35	Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu Asp Ile Thr Ala				
36	185	190	195		
37					
38	gcc agt gac cga tgg ctg ctg aac cat cac aag gac ctg gga ctc cgc				738
39	Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly Leu Arg				
40	200	205	210		
41					
42	ctc tat gtg gaa acc gcg gat ggg cac agc atg gat cct ggc ctg gct				786
43	Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly Leu Ala				
44	215	220	225		
45					
46	ggt ctg ctt gga cga caa gca cca cgc tcc aga cag cct ttc atg gta				834
47	Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe Met Val				
48	230	235	240		
49					
50	acc ttc ttc agg gcc agc cag agt cct gtg cgg gcc cct cgg gca gcg				882
51	Thr Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg Ala Ala				
52	245	250	255	260	
53					
54	aga cca ctg aag agg agg cag cca aag aaa acg aac gag ctt ccg cac				930
55	Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu Pro His				
56	265	270	275		
57					
58	ccc aac aaa ctc cca ggg atc ttt gat gat ggc cac ggt tcc cgc ggc				978

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1 Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser Arg Gly  
2 280 285 290  
3  
4 aga gag gtt tgc cgc agg cat gag ctc tac gtc aga ttc cgt gac ctt 1026  
5 Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Arg Phe Arg Asp Leu  
6 295 300 305  
7  
8 ggc tgg ctg gac tgg gtc atc gcc ccc cag ggc tac tct gcc tat tac 1074  
9 Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr  
10 310 315 320  
11  
12 tgt gag ggg gag tgt gct ttc cca ctg gac tcc tgt atg aac gcc acc 1122  
13 Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn Ala Thr  
14 325 330 335 340  
15  
16 aac cat gcc atc ttg cag tct ctg gtg cac ctg atg aag cca gat gtt 1170  
17 Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asp Val  
18 345 350 355  
19  
20 gtc ccc aag gca tgc tgt gca ccc acc aaa ctg agt gcc acc tct gtg 1218  
21 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val  
22 360 365 370  
23  
24 ctg tac tat gac agc aac aat gtc atc ctg cgt aaa cac cgt aac 1266  
25 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn  
26 375 380 385  
27  
28 atg gtg gtc aag gcc tgt ggc tgc cac tgaggccccg cccagcatcc 1313  
29 Met Val Val Lys Ala Cys Gly Cys His  
30 390 395  
31  
32 tgcttctact accttaccat ctggccgggc ccctctccag aggcagaaac ccttctatgt 1373  
33  
34 tatcatagct cagacagggg caaatgggagg cccttcactt cccctggcca cttectgcta 1433  
35  
36 aaattctggt ctttcccagt tcctctgtcc ttcatgggggt ttctggggcta tcaccccgcc 1493  
37  
38 ctctccatcc tccttacccca agcatagact gaatgcacac agcatccag agctatgcta 1553  
39  
40 actgagaggt ctggggtcag cactgaaggc ccacatgggg aagactgatc cttggccatc 1613  
41  
42 ctcagcccac aatggcaaat tctggatggt ctaagaagcc ctggaaatttc aaacttagatg 1673  
43  
44 atctgggctc tctgcaccat tcattgtggc agttgggaca ttttaggtta taacagacac 1733  
45  
46 atacaacttag atcaatgcat cgctgtactc cttgaaatca gagctagctt gtttagaaaaaa 1793  
47  
48 gaatcagagc caggtatagc ggtgcattgtc attaattccca gcgcctaaga gacagagaca 1853  
49  
50 ggagaatctc tggatgttca aggccacata gaaagagcct gtctcgggag caggaaaaaa 1913  
51  
52 aaaaaaaaaacg gaattc 1929  
53  
54  
55  
56  
57 SEQUENCE DESCRIPTION: SEQ ID NO:28:  
58

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1	GGCGCCGGCA GAGCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGGAGG TGGCACGGCA	60
2	GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCAGG AGGCCTGGA GCAAACAGCTC	120
3	CCACACCAGCA CCAAGCGGTG GCTGCAGGAG CTCGCCCATC GCCCCTGCGC TGCTCGGACC	180
4	GCGGCCACAG CGGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCGA GAGTCCCAGT	240
5	CCGCAGAGTA GCCCCGGGCT CGAGGCGGTG GCGTCCCGGT CCTCTCGTC CAGGAGCCAG	300
6	GACAGGTGTC GCGCGGCGGG GCTCCAGGGA CGCGCCTGTA GGCGGCTGC CGCCCGTCC	360
7	CGCCCCGCC CGCGCCCGC CGCCCGCCGA GCCCAGCCTC CTGGCGTC GGGCGTCCCC	420
8	AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC	480
9	CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG	528
10	Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu	
11	1 5 10	
12	GCG CTA TGC GCG CTG GGC GGG GGC CCC GGC CTG CGA CCC CCG CCC	576
13	Ala Leu Cys Ala Leu Gly Gly Pro Gly Leu Arg Pro Pro Pro	
14	15 20 25	
15	GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG	624
16	Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln	
17	30 35 40 45	
18	CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC	672
19	Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg	
20	50 55 60	
21	GCG CCA CCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG	720
22	Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	
23	65 70 75	
24	CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG	768
25	Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	
26	80 85 90	
27	CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT	816
28	Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val	
29	95 100 105	
30	AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG	864
31	Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp	
32	110 115 120 125	
33	AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC	912
34	Lys Glu Phe Arg Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val	
35	130 135 140	
36	ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC	960
37	Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu	
38	145 150 155	
39	AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC	1008
40	Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Gln Ser	

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1	160	165	170	
2				
3	AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT			1056
4	Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala			
5	175	180	185	
6				
7	GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC			1104
8	Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys			
9	190	195	200	205
10				
11	TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG			1152
12	Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu			
13	210	215	220	
14				
15	ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT			1200
16	Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly			
17	225	230	235	
18				
19	CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG			1248
20	Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg			
21	240	245	250	
22				
23	GCC AGT CCG AGT CCC ATC CGC ACC CCT CCG GCA GTG AGG CCA CTG AGG			1296
24	Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg			
25	255	260	265	
26				
27	AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC AAC CGA CTC			1344
28	Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu			
29	270	275	280	285
30				
31	CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG GTC TGC			1392
32	Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys			
33	290	295	300	
34				
35	CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC			1440
36	Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp			
37	305	310	315	
38				
39	TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG			1488
40	Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu			
41	320	325	330	
42				
43	TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC ATC			1536
44	Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile			
45	335	340	345	
46				
47	CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG			1584
48	Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala			
49	350	355	360	365
50				
51	TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC			1632
52	Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp			
53	370	375	380	
54				
55	AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC AAC ATG GTG GTC AAG			1680
56	Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg Asn Met Val Val Lys			
57	385	390	395	
58				

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1   GCC TGC GGC TGC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG  
2   Ala Cys Gly Cys His  
3   400

1723

Dated: October 20, 2006

/CONNIE WONG/

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